Playing with life expectancy and age-specific mortality rates. The mean method for indirect estimate.

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Abstract

Understanding mortality in detail, with respect to age, sex and country, is crucial for comprehending this complex phenomenon. Indirect estimation has emerged as a valid approach to derive analytical values from a synthetic index, allowing us to move beyond the narrow focus on life expectancy at birth that characterizes many forecasting models. By leveraging the resemblances in age-specific death rates among populations with similar life expectancies, it becomes feasible to reconstruct mortality across the entire lifespan. Essentially, this estimation is achieved by averaging age-specific death rates in the proximity of the provided life expectancy at birth. Preliminary results indicate minimal estimation errors and a coherent fit.

Keywords: indirect estimation; life expectancy; age-specific death rates; age patterns of mortality.

1 Introduction

Life expectancy at birth (usually denoted by e_0) is the most widely used index to summarise and communicate the longevity of a population or its subgroup. It represents the average number of years a newborn is expected to live, given the mortality conditions at a specific point in time. Its value is easily obtained and calculated, if the number of deaths and individuals by age is known. This has led to the development of forecasting models focused solely on estimating life expectancy (Pascariu et al., 2018; Raftery et al., 2014; Torri and Vaupel, 2012). These very parsimonious techniques have demonstrated high accuracy in predictions by taking advantage of the linear trend in life expectancy observed over the

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past 50 to 60 years (Oeppen and Vaupel, 2002; White, 2002). However, life expectancy at birth is a synthetic index, but mortality is a complex phenomenon and it is characterised by several components, such as example the level of infant and premature mortality, inequality at death (how much lifespan differs among individuals), skewness of adult mortality... On the one hand, therefore, e_0 was complemented with other values such as measures of lifespan variation (Hanada, 1983; Keyfitz, 1977; Tuljapurkar and Edwards, 2011; Vaupel and Romo, 2003), amount of premature mortality (Eurostat, 2009; Organization et al., 2018; Zanotto et al., 2021; Mazzuco et al., 2021), level of infant mortality (Canudas-Romo and Becker, 2011; Rabbi, 2013), which, however, were found to be linearly correlated with life expectancy at birth (see, for example, Nigri et al. (2022); Vaupel et al. (2011)). On the other hand, methodologies have been proposed that allow age patterns to be reconstructed from the value of life expectancy at birth. As a result, the need for indirect estimates arose: models that could reconstruct precise life tables based on a given level of e_0. For instance, the U.S. Census Bureau derives period age-specific death rates through projections of life expectancy at birth by sex and race (United States Census Bureau, 2014). Ševčíková et al. (2016) demonstrated how estimated projections for e_0 could be converted into age-specific death rates using the Lee-Carter model. A similar approach was proposed by Pascariu et al. (2020). Furthermore, Nigri et al. (2022) suggested employing a deep neural network model to obtain age-specific mortality from observed or predicted life expectancy. While the concept of modeling life tables is not new in the literature (see for example Coale and Demeny (1966)), this paper explores a new, simple, and parsimonious methodology for reconstructing age-specific mortality rates from life expectancy at birth. The underlying theoretical concept builds upon previous studies: identical average mortality levels, or equal life expectancy at birth, correspond to close curves of age-specific mortality rates across different years and countries. Consequently, populations with similar life expectancies at birth exhibit comparable death rates for each age group. To analyze mortality, we calculate the average death rate for each age class, drawing from populations closely matching the given value of e_0. In this paper, we introduce this straightforward yet effective approach for reconstructing life tables, demonstrating the relationships between age-specific death rates and life expectancy at birth. We also explore the method's advantages and disadvantages.

2 Method and Data

Separately for males and females, our proposed methodology, the MeaN (MN) method, consists of three consecutive steps. This gender diversification is essential due to the considerable differences in death rates at younger ages, even if their longevity is closer.

The first step involves establishing a value for life expectancy in year t, denoted as e_0^t. We then identify the years and countries (i.e. populations) in which life expectancy falls within the range of $[e_0^t - \delta, e_0^t + \delta]$.

In the second step, we calculate the expected values of the logarithm of age-specif death

rates, denoted as $\hat{m}_{x,e_0^t}$, using the following formula:

$$\log \hat{m}_{x_{e_0^t}} = \frac{\sum_{i=1}^{n} \log\left(m^i_{x_{(e_0^t-\delta, e_0^t+\delta)}}\right)}{n}, \tag{1}$$

Here, n represents the number of observed series, and x denotes ages ranging from 0 to 110.

In the final step, we employ splines (Hyndman and Ullah, 2007) to smooth out minor fluctuations in the rates, resulting in a more interpretable curve. The choice of δ is a crucial factor in this process. A too wide interval includes non-homogeneous populations, leading to increased estimation errors. Conversely, a very narrow interval may result in too few or no selected populations, impacting the estimate of $\hat{m}_x$. In this analysis, we have set δ to 0.1, striking a balance between a sufficiently large number of patterns and manageable error rates.

To validate our methodology, we utilized mortality tables from the Human Mortality Database (HMD) Human Mortality Database (2023). This database ensures high data quality and comparability across different populations. We specifically applied the method to reconstruct Italian women's death rates from 1950 to 2020, a period that covers diverse longevity trajectories. Italy's demographic transition, delayed compared to other countries but followed by a rapid increase in life expectancy, makes it one of Europe's longest-living nations. Additionally, the drawback of life expectancy due to the impact of the COVID-19 pandemic is noteworthy.

For each year t in the series, we matched female populations that reported before the year t an e_0 within $[e_0^t - 0.1, e_0^t + 0.1]$. Only the years before t are considered because we mimic the only information available at that time. This methodology does not require any training. Unlike models that rely on time windows to estimate parameters, the proposed technique simply selects sets of similar specific rates by considering a reasonable range, encompassing all years and countries for which mortality tables are available. Equation 1 was applied to the selected death rate series, and after smoothing with splines, we compared the results with the actual values reported in the initial life table. To assess the model's accuracy, we calculated the relative difference between observed and estimated values using the equation:

$$\epsilon_{x_{e_0^t}} = \frac{\log m_{x_{e_0^t}} - \log \hat{m}_{x_{e_0^t}}}{\log m_{x_{e_0^t}}}. \tag{2}$$

To summarize the performance, we computed year-by-year the root mean square error (RMSE):

$$RMSE_t = \sum_{x=1}^{\omega} \sqrt{\frac{\left(\log m_{x_{e_0^t}} - \log \hat{m}xe_0^t\right)^2}{m_\omega}}, \tag{3}$$

with m_ω represents for the number of estimated age classes. Equations 3 is also particularly useful for determining the optimal value for δ.

3 Results

Figure 1 provides a visual representation of female age-specific death rates (on a logarithmic scale) for four selected years, offering an insightful overview of the model's performance. The highest error (i.e. $RMSE_t$) is observed in 1952, with a value of 0.1018. It's worth

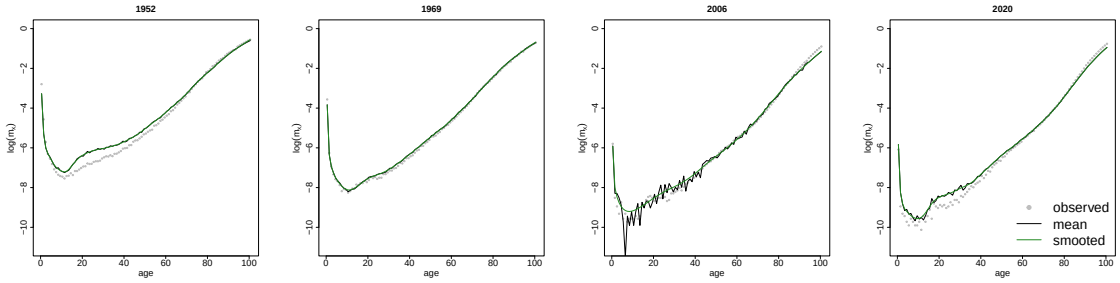

Figure 1: Estimated age-specific log-mortality rates $\log(m_x)$ for Italian women.

noting that 13 populations were selected during this year (an amusing coincidence for those who are superstitious). The discrepancies between estimated and observed death rates are predominantly concentrated between the ages of 15 and 40, where the estimated curve consistently overestimates mortality. In contrast, the best model performance is observed in 1969, with 30 matched populations and a mean error of 0.0088. During this year, the predicted curve closely aligns with the actual values, showcasing the model's accuracy. Between 2000 and 2019, Italy experienced a significant surge in life expectancy, particularly among women. This period provides an intriguing case study for observing how the methodology adapts. Given Italy's status as one of the world's longevity leaders, finding reference populations can be challenging. In 2006, only one population falls within the interval $[e_0^{2006} - 0.1, e_0^{2006} + 0.1]$, yet the error remains minimal at 0.0476. This is primarily attributed to the smoothing effects of splines, which eliminate irregularities and result in a curve that consistently mirrors the actual data. While having only a single reference population may seem inadequate, it is the proximity of life expectancy values that matters most in this context, ensuring precise estimates of death rates. The final graph pertains to 2020, a year affected by the COVID-19 pandemic, which caused a decline in life expectancy to levels last seen before 2010[1]. In this case, 16 populations exhibited similar life expectancies, resulting in an error of 0.0875. Compared to other years with a

[1]In 2019, the life expectancy of Italian women stood at 85.41. The subsequent year witnessed a nearly one-year drop to 84.47, a similar value to 2010 (84.52).

similar number of series, this error is higher. It could be attributed to the unique mortality pattern associated with the pandemic, which is difficult to estimate.

A comprehensive overview of the ifferences between estimates and observed death rate can be found in Figure 2. In most years, the errors are quite small, typically within the

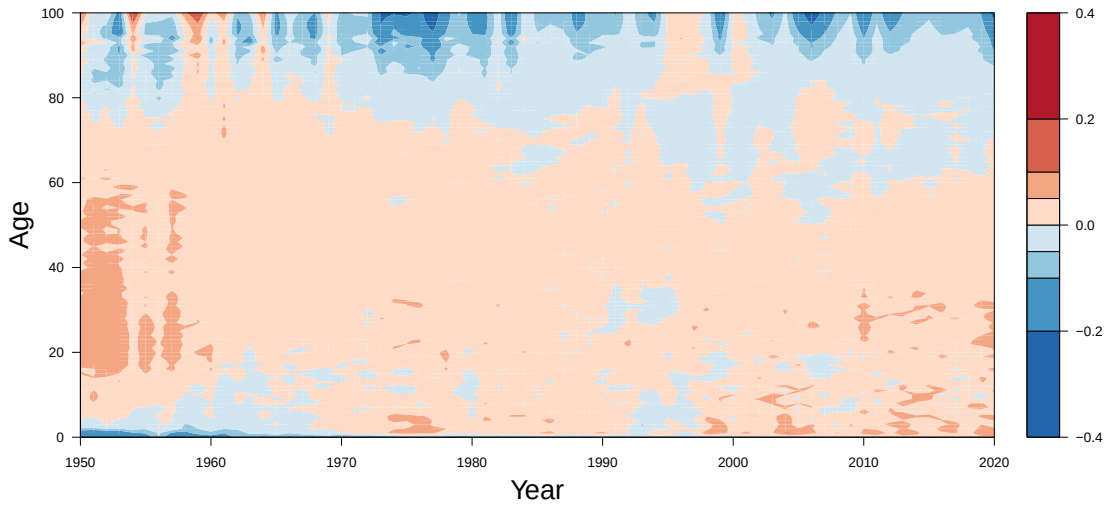

Figure 2: Relative differences (log scale) between estimated and observed age-specific death rates for the MN method. Red hues indicate overestimated mortality, while blue hues indicate underestimation.

range of -0.05 to +0.05. The model tends to overestimate mortality between ages 0 and 75, but underestimates mortality at older ages. The most significant differences are observed beyond the age of 80, with $\epsilon_{x_{e_0^t}}$ exceeding 0.1. High overestimates ($0.05 < \epsilon_{x_{e_0^t}} < 0.1$) are observed in the first years between the ages 15 and 50.

Figure 3 presents a comprehensive view of the relationship between the number of extracted populations, estimation errors, and life expectancy values. For the years preceding 1960, the average errors fall within the range of 0.0237 to 0.1018, with the number of selected populations spanning from 3 to 13. Notably, these errors primarily stem from age groups between 15 and 50, where the model consistently overestimates mortality (refer to Figure 2). Subsequently, as life expectancy increases, predominantly attributed to reductions in infant mortality, we witness a progressive rise in the number of selected series, peaking at 32. This rise is accompanied by a proportional decrease in average errors. The 2000s marked a remarkable period in Italy's demographic landscape, characterized by an exceptional surge in longevity. This phenomenon results in a decline in the number of extracted series, leading to an increase in errors. Nevertheless, a discernible variability re-

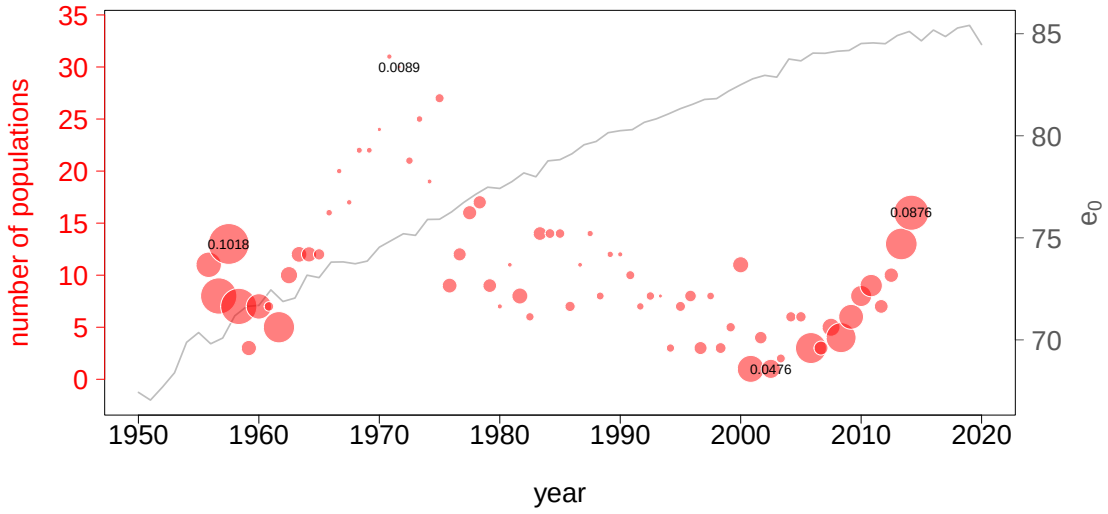

Figure 3: Number of matched series per year. The size of the dots represent the observed root mean square error $RMSE_t$. The grey line shows the trend in life expectancy for Italian women.

mains. In general, a larger number of death rate series appears to contribute to a reduction in errors.

4 Discussion and Future Devepolments

The foundational concept underpinning the development of the MN method for the indirect estimation of age-specific death rates is very simple: populations with similar mortality patterns are associated with the same life expectancy values. Consequently, decomposing mortality becomes a matter of calculating the average death rates for populations that share commonalities in terms of longevity. To validate the model's effectiveness, we examined the mortality data of Italian women from 1950 to 2020. Overall, the MN method appears to provide adequate estimations of age-specific death rates, with notably small errors, particularly in the period spanning from 1960 to the 2000s. While there is a noticeable reduction in errors as the number of selected populations increases, there are instances where proximity to the life expectancy of interest appears to hold greater significance. In a comparative context, the MN method demonstrates lower errors when applied to Italian women, in contrast to the model proposed by Nigri et al. (2022), which, so far, has shown the best performance. One key advantage of our approach is its lack of training time, as populations with similar life expectancy values are selected on a case-by-case basis.

However, countries with life expectancies that teeter on the borderlines, be it higher or lower, pose more significant challenges. In such cases, the available reference populations become limited, increasing the risk of systematically underestimating or overestimating mortality. It is worth noting that even more advanced models, while capable of extrapolating trends (which the MN method cannot do), are not immune to this type of risk when estimating death rates for very low or exceptionally long-lived populations. To gain a deeper understanding, a systematic comparison with other indirect estimation models is essential. Further, performance analysis should be extended to include other countries that hold significance in mortality trajectories, such as Japan with its exceptionally high life expectancies, the United States characterized by stagnation and slow improvements in life expectancy, and Russia with the highest mortality at younger ages and lower life expectancy.. An additional question worth exploring is whether there exists an optimal level for δ and whether this level should be standardized or tailored to individual countries or specific life expectancy values. These aspects hold the potential for further refinement and enhancement of the MN method.

In conclusion, the MN method has demonstrated its capacity for robust and reliable indirect estimations of death rates. The competitive edge it holds over existing models is further underscored by its swift adaptability without the need for extensive training. As we expand our horizons to consider other countries with distinct demographic profiles, we are presented with the opportunity to further validate the MN method's universal applicability.

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